

# A Decade with the Human Genome Sequence: Charting a Course for Genomic Medicine

## Symposium Microblog Transcript

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| At 2011-02-07 19:46:12, [nihlibrarybioinformatics] said:  
| We're looking forward to the symposium on Friday.

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| At 2011-02-11 13:05:58, [benstanfield] said:  
| Good morning, everyone! If you need any help using the site  
| today, you can let me know by sending me a message that includes  
| @benstanfield, or you can use the hashtag #tech support. But  
| before you can do either of those, you'll need to register with  
| the site by visiting <http://genomics2011.com/main/register> . You  
| can also sign in with an openID account if you have one. Just  
| visit <http://genomics2011.com/main/openid> You should receive an  
| email asking you to confirm your email address a few seconds  
| after registering. If you don't, it might be hiding in your spam  
| folder.

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| At 2011-02-11 13:35:08, [lowercase] said:  
| Are speaker materials available?

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| At 2011-02-11 13:36:37, [lowercase] said:  
| video feed is stuck

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| At 2011-02-11 13:40:31, [larrythompson] said:  
| We are working on the webcast feed. Should be fixed shortly.

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| At 2011-02-11 13:48:28, [lowercase] said:  
| Please let us all know when to expect a working feed so we can go  
| do something else.

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| At 2011-02-11 13:52:45, [drjonboyg] said:  
| Short speaker introductions. Good idea.

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| At 2011-02-11 13:53:24, [drjonboyg] said:  
| @benstanfield Is there a way to change my avatar in iOS?

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| At 2011-02-11 13:57:43, [benstanfield] said:

| @drjonboyg Unfortunately, I don't think so. However, if you have  
| a gravatar account, you can set that from an IOS device. Click on  
| "account" at the top of the page, then email and make sure your  
| email address is confirmed. Then click on "avatar" and at the  
| bottom of the page, you can click "add" in the gravatar section.

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| At 2011-02-11 14:00:59, [tf] said:

| what do people think of strategic plan?

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| At 2011-02-11 14:04:00, [ctls4cancer] said:

| Perhaps linking it to funding levels would put more teeth in it

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| At 2011-02-11 14:06:01, [krisw] said:

| @ctls4cancer The plan covers the entire field of genomics, not  
| just what NHGRI might fund. However, efforts have already started  
| at NHGRI to detemrine priorities and develop new initiatives.

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| At 2011-02-11 14:10:30, [tf] said:

| i like the idea of a "grand plan" but would like to see more "arc  
| to clinical" small projects. seems like significant benefits to  
| health care should come far sooner than 2020...

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| At 2011-02-11 14:10:33, [manoli] said:

| The video and audio are out of sync

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| At 2011-02-11 14:11:39, [manoli] said:

| @ctls4cancer During the planning meetings, they very specifically  
| asked us to not include funding constraints in the discussions,  
| which was a challenge

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| At 2011-02-11 14:15:15, [ctls4cancer] said:

| I'm thankful for Francis' big picture view of development

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| At 2011-02-11 14:17:15, [dnawriter] said:

| @lowercase feed should be fine now.

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| At 2011-02-11 14:17:51, [dnawriter] said:

| Also, speaker materials should be up on genome.gov later. Can't  
| say exactly when.

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| At 2011-02-11 14:18:46, [bsw] said:  
| how can i view the conference? please help me get on!

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| At 2011-02-11 14:23:07, [krisw] said:  
| <http://videocast.nih.gov/>

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| At 2011-02-11 14:24:11, [bsw] said:  
| when i FINALLY get the video screen, it is black, and says "live  
| broadcast - paused"; this is not changed by hitting any of the  
| buttons. is there any way to see this conference? or is it not  
| working for anyone? is there a phone number to call, to talk to  
| an actual humanoid?

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| At 2011-02-11 14:28:10, [benstanfield] said:  
| @bsw The videocast currently has over 500 viewers, so it's  
| definitely working for some people. We've gotten a variety of  
| reports on the quality of the stream, from excellent, to audio  
| out of sync, to picture refreshing only ever few seconds, but the  
| stream is up and working for most people. The videocast team at  
| NIH has a contact page here: <http://videocast.nih.gov/ContactUs/>  
| with a section on #techsupport. They might be able to help.

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| At 2011-02-11 14:28:17, [manoli] said:  
| @bsw It's been working continuously here at MIT

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| At 2011-02-11 14:28:37, [bsw] said:  
| please, is there a phone number to call, to talk to a real person,  
| to get help for logging onto this conference

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| At 2011-02-11 14:30:13, [drjonboyg] said:  
| My one issue with Moore's law and sequencing: Moore's law applies  
| to transistors on a chip, the basic technology stays the same.  
| Sequencing costs are coming down by moving to totally new  
| platforms and technologies. Still, the end result is the same, I  
| suppose.

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| At 2011-02-11 14:30:54, [manoli] said:  
| Cute green/yellow picture of coding vs. non-coding from the  
| 4-yeast paper ;-)

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| At 2011-02-11 14:31:06, [benstanfield] said:

| Videos of all of the talks will be archived and available for  
| viewing after the symposium, so if you're one of the few unable  
| to connect this morning, you'll still have a chance to watch all  
| of the talks.

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| At 2011-02-11 14:31:07, [bsw] said:  
| @manoli - please - how did you get on? i get only a black  
| screen saying paused

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| At 2011-02-11 14:32:09, [manoli] said:  
| @bsw If you click on this, it will open in a separate realplayer  
| window <http://videocast.nih.gov/ram/nhgri021111.ram>

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| At 2011-02-11 14:33:20, [drjonboyg] said:  
| @bsw Have you tried a different browser? Or restarting your  
| browser?

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| At 2011-02-11 14:33:29, [bsw] said:  
| @benstanfield can you please tell me how to see something other  
| than a black screen with no sound, saying pause

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| At 2011-02-11 14:35:38, [bsw] said:  
| @drjonboyg both Safari and Firefox give the same black screen,  
| saying paused

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| At 2011-02-11 14:37:40, [krisw] said:  
| @bsw Try contacting the NIH Help Desk:  
| <http://videocast.nih.gov/ContactUs/Default.aspx?bhcp=1>

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| At 2011-02-11 14:43:25, [benstanfield] said:  
| @larrythompson Webcast feed just markedly improved for me. Looks  
| like things are getting better.

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| At 2011-02-11 14:51:18, [manoli] said:  
| Eric Lander making a very strong case for disease studies

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| At 2011-02-11 14:52:49, [manoli] said:  
| First explain the biology, then understand the heritability.  
| Drugs can have strong effect despite small heritability. Parallel  
| pathways change the denominator

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| At 2011-02-11 14:53:52, [dnawriter] said:  
| I could listen to Lander speak all day. He's like a really good  
| PBS special.

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| At 2011-02-11 14:56:25, [alice] said:  
| Make sure to check out Eric Lander's article in this week's issue  
| of Nature

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| At 2011-02-11 14:57:44, [manoli] said:  
| @alice  
| [http://www.nature.com/nature/journal/v470/n7333/full/nature09792.](http://www.nature.com/nature/journal/v470/n7333/full/nature09792.html)  
| html

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| At 2011-02-11 15:05:14, [dnawriter] said:  
| fly genomics. cool.

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| At 2011-02-11 15:06:01, [manoli] said:  
| Very good question on analysis by Deana, answered by cost of  
| sample preparation, storage, but computational biology aspect  
| should be emphasized more

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| At 2011-02-11 15:06:40, [manoli] said:  
| Sean Eddy on comparative genomics and the Rosetta Stone

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| At 2011-02-11 15:07:56, [manoli] said:  
| "source code" to the wonderful creatures ;-)

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| At 2011-02-11 15:08:08, [tf] said:  
| why do speakers not thank/acknowledge funding sources... or did i  
| miss?

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| At 2011-02-11 15:09:24, [manoli] said:  
| Eddy: celera coffee mug = viking enemy skull

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| At 2011-02-11 15:14:23, [wyattsgirl] said:  
| #NHGRI: Eddy- pattern of conservation is also informative.

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| At 2011-02-11 15:14:32, [krisw] said:  
| @tf I think the talks that have occurred so far weren't about

| specific work that the speakers have done under particular  
| funding.

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| At 2011-02-11 15:15:10, [bsw] said:

| @krisw thanks so much! that page gave phone numbers, one of  
| which was answered by a live person, who got me to another  
| person, who said the lines were over-subscribed, so were showing  
| only black to us "extras". and they finally put on ore capacity.  
| so i got on now. yay!!

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| At 2011-02-11 15:17:06, [krisw] said:

| Genome scientists = computer hackers

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| At 2011-02-11 15:17:06, [manoli] said:

| Decoding typed characters based on audio pattern of spacings.  
| Neat idea, worth demonstrating

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| At 2011-02-11 15:18:00, [manoli] said:

| Lagging strand more prone to deamination of C -> depletion on  
| lagging strand

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| At 2011-02-11 15:18:42, [manoli] said:

| Mutational biases have already been used for gene finding (FEAST)

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| At 2011-02-11 15:18:46, [drjonboyg] said:

| RT @manoli Very good question on analysis by Deana, answered by  
| cost of sample preparation, storage, but computational biology  
| aspect should be emphasized more

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| At 2011-02-11 15:22:21, [manoli] said:

| Surprising that no new structural classes were found (and a tid  
| bit disappointing... could we have found them all??)

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| At 2011-02-11 15:26:23, [dnawriter] said:

| Blast tool most important tool in comp biology...

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| At 2011-02-11 15:28:15, [manoli] said:

| By the way, here's cracking typing by listening to keyboard:  
| [http://www.cs.berkeley.edu/~tygar/papers/Keyboard\\_Acoustic\\_Emanat  
| ions\\_Revisited/tiss.preprint.pdf](http://www.cs.berkeley.edu/~tygar/papers/Keyboard_Acoustic_Emanations_Revisited/tiss.preprint.pdf)

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| At 2011-02-11 15:33:10, [david] said:  
| The symposium video is now available in Flash, which should help  
| with the sync problems, etc.

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| At 2011-02-11 15:33:25, [david] said:  
| Here's the Flash URL:  
| <http://videocast.nih.gov/live-lb.asp?live=9981>

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| At 2011-02-11 15:37:16, [nihlibrarybioinformatics] said:  
| Nice graphic from Eddy of BLAST as an approximation to a profile  
| HMM

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| At 2011-02-11 15:46:49, [themichaelbk] said:  
| @dnawriter Yes, same here. He's a rare example of someone who is  
| simultaneously brilliant, enthusiastic and impassioned about his  
| topic of expertise but can also make it accessible to the lay  
| person. I thoroughly enjoyed listening to him speak.

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| At 2011-02-11 15:50:32, [dgmacarthur] said:  
| Ouch! Jennifer Wagner from Duke has a scathing critique of the  
| NHGRI strategic plan, which she describes as an "EPIC FAIL":  
| <http://bit.ly/fFojtG>

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| At 2011-02-11 16:08:10, [tf] said:  
| i don't see these talks (so far) as adding up to the title.

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| At 2011-02-11 16:12:55, [dnawriter] said:  
| @tf Most of the talks right now are about the last decade of  
| research, but I think we'll see more about the future of genomics  
| in upcoming talks.

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| At 2011-02-11 16:23:48, [nihlibrarybioinformatics] said:  
| Yes, Eddy's talk is the kind that inspires one to go back and  
| read more of his papers.

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| At 2011-02-11 16:28:31, [nihlibrarybioinformatics] said:  
| Maybe we will be using some super fast version of HMMER more  
| often than BLAST one day.

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| At 2011-02-11 16:32:31, [marivas] said:

| fascinating findings on kindreds

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| At 2011-02-11 16:36:11, [wyattsgirl] said:

| @dgmacarthur her view is clearly not one that looks at the entire  
| strategic plan but one component... not sure that narrow analysis  
| is fair to call the entire plan an epic fail

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| At 2011-02-11 16:49:11, [nihlibrarybioinformatics] said:

| Regarding the kindreds, is Lifton's diagram of nine generations  
| around a rectangle a common representation?

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| At 2011-02-11 16:55:52, [marivas] said:

| it is an unusual kindred diagram...

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| At 2011-02-11 18:22:40, [dnawriter] said:

| It's cool to hear a real patient's perspective. Good for you Rick  
| DelSontro

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| At 2011-02-11 18:31:33, [alice] said:

| The panel has already alluded to some important current issues in  
| genomics- return of results and confidentiality

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| At 2011-02-11 19:07:23, [genmol] said:

| I see with very much concern, that a computer algorithm will  
| interpret genetic results instead of a highly trained  
| professional. Sometimes, not even these professionals can answers  
| those questions, and most of the times those results are patient  
| specific, thus very difficult to address. I do not believe that a  
| web-based software would be able to give a real-life accurate  
| interpretation of those results.

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| At 2011-02-11 19:10:14, [manoli] said:

| Brad Bernstein on surveying human epigenomes

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| At 2011-02-11 19:22:07, [manoli] said:

| Very nice intro to recent findings in epigenomics

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| At 2011-02-11 19:26:16, [manoli] said:

| Clustering cell types using principle components of  
| H3K4me1/me3/K3K36/H3K27me3

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| At 2011-02-11 19:28:34, [manoli] said:  
| ENCODE project 9 cell types x 9 marks

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| At 2011-02-11 19:45:21, [nihlibrarybioinformatics] said:  
| Bernstein's proposal to use epigenomic to triage variants found  
| in GWAS studies seems very powerful. It could be useful in

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| At 2011-02-11 19:46:08, [nihlibrarybioinformatics] said:  
| It could be useful in many sequencing studies.

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| At 2011-02-11 19:47:50, [manoli] said:  
| @nihlibrarybioinformatics A public track with the chromatin state  
| annotation for all nine cell types will soon be available on the  
| UCSC browser

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| At 2011-02-11 19:52:46, [nihlibrarybioinformatics] said:  
| @manoli We look forward to telling our users about it.

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| At 2011-02-11 20:05:20, [tf] said:  
| While all these presentations have been brilliant, I continue to  
| feel that today should be much more about going forward -- NIH,  
| give me a better/brighter picture of real progress towards  
| genomic medicine and a shift of investment/effort from mostly  
| pure science to mostly translation to health care. When/how will  
| we see genomics move the meters of mortality rates and health  
| care costs? What can/should health care professionals and market  
| players do to accelerate the advance? And can/how these  
| investments spur economic development, new businesses, and  
| non-government jobs?

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| At 2011-02-11 21:16:40, [beckerjes] said:  
| AGREED! More open publishing!

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| At 2011-02-11 21:23:58, [drjonboyg] said:  
| I dont know what Amy Harmon is talking about. NIH research has to  
| be published as open access, or the papers have to be deposited  
| in NLM's open access database by law (signed in 2007 no less):  
| [http://www.sciencecodex.com/public\\_access\\_mandate\\_made\\_law](http://www.sciencecodex.com/public_access_mandate_made_law)

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| At 2011-02-11 21:33:02, [beckerjes] said:  
| @drjonboyg @drjonboyg There is a \*lot\* of research--not just in

| the genetics/genomics fields--that is stuck behind a pay-wall  
| (almost anything published by Elsevier comes to mind...). I'm  
| aware of the public access laws (and of Congress's attempts to  
| repeal them) for NIH-funded research, but there is a lot more to  
| be done. She has a very good point and I do not think it should  
| be dismissed.

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|At 2011-02-11 21:38:26, [drjonboyg] said:

| @beckerjes I have been as big an advocate for one access as  
| anyone I know, all the way back to grad school in the 1990s. But  
| it's just not factually correct to call NIH out for not using  
| open access when there is a legal mandate to do exactly the  
| opposite.

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|At 2011-02-11 21:45:46, [beckerjes] said:

| @drjonboyg Not all research is funded by the NIH; not everyone is  
| covered by the open access laws. My comment is more general,  
| covering all of scientific research in general. I agree that the  
| NIH is actually very good about this.